



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Goeddel, David V. Rothe. Mike
- (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
- (iii) NUMBER OF SEQUENCES: 59

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 460 Point San Bruno Blvd
- (C) CITY: South San Francisco
- (D) STATE: California(E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 07-Jan-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dreger, Ginger R.
- (B) REGISTRATION NUMBER: 33,055
- (C) REFERENCE/DOCKET NUMBER: P0897C2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-3216
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50 GGCGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700 CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900 GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350 CGGCTGCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400 CCTACGTCAA AGATGACACA ATGTTCCTCA AATGCATTGT GGACACTAGT 1450 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500 GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550 CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600 GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650 GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700 GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750 GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800 AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850



TGGAAAAATG CCCCCATCTC TCTGTTCAGA CTCAAAACTA GAACCACAGG 1900
GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950
CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000
TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050
ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAA 2088

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly

1 5

10

15

Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu

20

25

30

Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp

35

40

45

Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser

50

55

60

Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala

65

70

75

Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe

80

85

90

Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln

95

100



Ser Ser I	His Leu Tyr Le	u Leu Leu Ala	Val Leu Lys Glu Trp Lys
	110	115	120
Ser Ser F	Pro Gly Ser As	n Leu Gly Ser	Ala Pro Met Ala Leu Glu
	125	130	135
Arg Asn	Leu Ser Glu L	eu Gln Leu Gl	n Ala Ala Val Glu Ala Thr
	140	145	150
Gly Asp	Leu Glu Val A	asp Cys Tyr Ai	rg Ala Pro Cys Cys Glu Ser
	155	160	165
Gln Glu	Glu Leu Ala L	eu Gln His Le	u Val Lys Glu Lys Leu Leu
	170	175	180
Ala Gln	Leu Glu Glu L	ys Leu Arg Va	al Phe Ala Asn Ile Val Ala
	185	190	195
Val Leu	Asn Lys Glu V	al Glu Ala Se	r His Leu Ala Leu Ala Ala
	200	205	210
Ser Ile H	is Gln Ser Gln	Leu Asp Arg	Glu His Leu Leu Ser Leu
	215	220	225
Glu Gln	Arg Val Val G	lu Leu Gln Gli	n Thr Leu Ala Gln Lys Asp
	230	235	240
Gln Val l	Leu Gly Lys L	eu Glu His Sei	Leu Arg Leu Met Glu Glu
	245	250	255
Ala Ser F	Phe Asp Gly Tl 260	nr Phe Leu Trp 265	Lys Ile Thr Asn Val Thr 270
Lys Arg	Cys His Glu So 275	er Val Cys Gly 280	Arg Thr Val Ser Leu Phe 285
Ser Pro A	Ala Phe Tyr Th	r Ala Lys Tyr	Gly Tyr Lys Leu Cys Leu
	290	295	300
Arg Leu	Tyr Leu Asn C	Gly Asp Gly Se	er Gly Lys Lys Thr His Leu 315

Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu 320 325 330

Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln 335 340 345

Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser 350 355 360

Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser 365 370 375

Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys 380 385 390

His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val 395 400 405

Asp Thr Ser Ala 409

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2121 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50
GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100
CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150
CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200
CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250



CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300 TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCGCAG AGAGGTGGAG 350 AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400 GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450 AGTGTCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550 ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650 TTTCAGGACC ATGTTAGAGC ATGCAGCAAA TGCCGGGTTC TCTGCAGATT 700 CCACACCGTT GGCTGTTCAG AGATGGTGGA GACTGAGAAC CTGCAGGATC 750 ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800 TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900 TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000 TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050 TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100 GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150 CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200 GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250 GGGCGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300

TGATGCTCTG TTGCAGTGGC CTTTTAATCA GAAGGTAACA TTGATGTTGC 1350 TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400 ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450 CTGCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500 TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550 TAGCCACCCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600 CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650 GGAGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700 AGCCTCCAGT TGGCCTTCAG CTGGCAAACT GAGTTGGACG GTCCACTGAG 1750 CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800 AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGAC CTGTAGGTGG 1850 GTGCTCAGAA AGGGCCTCTC CAGAGAGAGT CTCAAGAGCT GCAGCAGGAG 1900 CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950 ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000 CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050 TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100 CGACAAAAA AAAAAAAAA A 2121

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

- Met Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu 1 5 10 15
- Gln Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala 20 25 30
- Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe 35 40 45
- Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser 50 55 60
- Ile Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu 65 70 75
- Gly Leu Tyr Glu Glu Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala 80 85 90
- Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala 95 100 105
- Val Cys Pro Asn Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu
 110 115 120
- Tyr Glu Ser Cys His Glu Gly Leu Cys Pro Phe Leu Leu Thr Glu
 125 130 135
- Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Ser Glu Lys Glu His 140 145 150
- His Thr Glu Gln Glu Cys Pro Lys Arg Ser Leu Ser Cys Gln His 155 160 165
- Cys Arg Ala Pro Cys Ser His Val Asp Leu Glu Val His Tyr Glu 170 175 180
- Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys 185 190 195

Lys Ile Pro Arg Glu	Thr Phe Glr	n Asp His Val Ai	rg Ala Cys Ser
200	205	210	

- Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu 215 220 225
- Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu 230 235 240
- Arg Glu His Leu Ala Leu Leu Ser Ser Phe Leu Glu Ala Gln 245 250 255
- Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln 260 265 270
- Arg Cys Gln Ile Leu Glu Gln Lys Ile Ala Thr Phe Glu Asn Ile 275 280 285
- Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala 290 295 300
- Glu Ala Cys Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu 305 310 315
- Ala Leu Ser Asn Lys Val Gln Gln Leu Glu Arg Ser Ile Gly Leu 320 325 330
- Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys Val Ser Glu Leu 335 340 345
- Glu Val Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys Ile Ser Asp 350 355 360
- Phe Thr Arg Lys Arg Gln Glu Ala Val Ala Gly Arg Thr Pro Ala 365 370 375
- Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys Met 380 385 390
- Cys Leu Arg Val Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr 395 400 405

His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala 410 415 420 Leu Leu Gln Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu 430 435 Asp His Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp 445 450 Val Thr Ser Ser Ser Phe Gln Arg Pro Val Ser Asp Met Asn Ile 455 460 465 Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala 480 470 475 Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile 485 490 495 Val Asp Leu Thr Gly Leu 500 501 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 amino acids (B) TYPE: Amino Acid (D) TOPOLOGY: Linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: Asp Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe 1 5 10 15 Leu Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr 20 25 30 His Leu Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His 35 40 44

(2) INFORMATION FOR SEQ ID NO:6:

(A) I (B) 7	QUENCE CHA LENGTH: 47 a FYPE: Amino FOPOLOGY:	amino acids Acid	TICS:
(xi) SEC	QUENCE DES	SCRIPTION:	SEQ ID NO:6:
Glu Leu 1	Ser Cys Ser II	e Cys Leu G 10	lu Pro Phe Lys Glu Pro Val 15
Thr Thr	Pro Cys Gly H 20	lis Asn Phe (25	Cys Gly Ser Cys Leu Asn Glu 30
Thr Trp	Ala Val Gln G 35	ly Ser Pro T	yr Leu Cys Pro Gln Cys Arg 45
Ala Val 47			
(2) INFO	RMATION F	OR SEQ ID	NO:7:
(A) I (B) T	UENCE CHA LENGTH: 44 a TYPE: Amino TOPOLOGY:	amino acids Acid	TICS:
(xi) SEC	QUENCE DES	SCRIPTION:	SEQ ID NO:7:
Leu Leu 1	Arg Cys His I 5	le Cys Lys A 10	asp Phe Leu Lys Val Pro Val
Leu Thr	Pro Cys Gly F 20	Iis Thr Phe C 25	Cys Ser Leu Cys Ile Arg Thr 30
His Leu	Asn Asn Gln l 35		Pro Leu Cys Leu Phe Glu 44
(2) INFO	RMATION F	OR SEQ ID	NO:8:
` '	UENCE CHA LENGTH: 44 a		TICS:



• ,	YPE: Amino COPOLOGY: 1		
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:8:
Ala Phe	Arg Cys His V 5	al Cys Lys A 10	sp Phe Tyr Asp Ser Pro Met 15
Leu Thr	Ser Cys Asn F 20	His Thr Phe Co	ys Ser Leu Cys Ile Arg Arg 30
Cys Leu	Ser Val Asp S 35	•	ro Leu Cys Arg Ala Thr 4
(2) INFO	RMATION FO	OR SEQ ID N	O:9:
(A) L (B) T	UENCE CHA ENGTH: 45 a YPE: Amino OPOLOGY: 1	mino acids Acid	ICS:
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:9:
Ser Ile Se	er Cys Gln Ile 5	Cys Glu His 1	Ile Leu Ala Asp Pro Val 15
Glu Thr	Asn Cys Lys F 20	His Val Phe C	ys Arg Val Cys Ile Leu Arg 30
Cys Leu	Lys Val Met (35	Gly Ser Tyr C	ys Pro Ser Cys Arg Tyr Pro 45
(2) INFOI	RMATION FO	OR SEQ ID N	O:10:
(A) L (B) T	UENCE CHA ENGTH: 45 a YPE: Amino . OPOLOGY: 1	mino acids Acid	ICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Val	Thr Cys Pro Il	e Cys Leu As _j	p Pro Phe Val Glu Pro Val
	5	10	15
Ser Ile G	lu Cys Gly Hi	s Ser Phe Cys	Gln Glu Cys Ile Ser Gln
	20	25	30
Val Gly	Lys Gly Gly C	Gly Ser Val Cy	vs Ala Val Cys Arg Gln Arg
	35	40	45
(2) INFO	RMATION FO	OR SEQ ID N	O:11:
(A) L (B) T	UENCE CHA ENGTH: 46 a YPE: Amino OPOLOGY: I	nmino acids Acid	ICS:
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:11:
Glu Leu	Met Cys Pro I	le Cys Leu As	sp Met Leu Lys Asn Thr Met
1	5	10	15
Thr Thr I	Lys Glu Cys L	eu His Arg Pl	ne Cys Ser Asp Cys Ile Val
	20	25	30
Thr Ala l	Leu Arg Ser G	ely Asn Lys G	lu Cys Pro Thr Cys Arg Lys
	35	40	45
Lys 46			
(2) INFO	RMATION FO	OR SEQ ID N	O:12:
(A) L (B) T	UENCE CHA ENGTH: 50 a YPE: Amino OPOLOGY: 1	mino acids Acid	ICS:
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:12:
Glu Val 7	Γhr Cys Pro Il	e Cys Leu Glu	ı Leu Leu Lys Glu Pro Val
	5	10	15

Ser Ala A	sp Cys Asn F	25	30
Asn Tyr (Glu Ser Asn A 35	arg Asn Thr A 40	sp Gly Lys Gly Asn Cys Pro 45
Val Cys A	Arg Val Pro 50		
(2) INFOR	RMATION FO	OR SEQ ID N	O:13:
(A) L1 (B) T	JENCE CHA ENGTH: 47 a YPE: Amino A OPOLOGY: I	mino acids Acid	ICS:
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:13:
Glu Thr T 1	Thr Cys Pro V	al Cys Leu G	In Tyr Phe Ala Glu Pro Met 15
Met Leu A	Asp Cys Gly I 20	His Asn Ile Cy 25	ys Cys Ala Cys Leu Ala Arg 30
Cys Trp C	Gly Thr Ala G 35	lu Thr Asn Va 40	al Ser Cys Pro Gln Cys Arg 45
Glu Thr 47			
(2) INFOR	MATION FO	OR SEQ ID N	O:14:
(A) LI (B) T	JENCE CHA ENGTH: 48 a YPE: Amino A OPOLOGY: I	mino acids Acid	ICS:
(xi) SEQ	UENCE DES	CRIPTION: S	SEQ ID NO:14:
Phe Gln L	eu Cys Lys II 5	e Cys Ala Gl	u Asn Asp Lys Asp Val Lys 15

Ile Glu P	ro Cys Gly Hi 20	s Leu Met Cy 25	rs Thr Ser Cys Leu Thr Ser 30
Trp Gln (Glu Ser Glu G 35	ly Gln Gly Se 40	er Ser Gly Cys Pro Phe Cys 45
Arg Cys	Glu		
(2) INFOI	RMATION FO	OR SEQ ID N	IO:15:
(A) L (B) T	UENCE CHA ENGTH: 28 a YPE: Amino . OPOLOGY: 1	mino acids Acid	TICS:
(xi) SEQ	UENCE DES	CRIPTION:	SEQ ID NO:15:
Gly Gly I	Phe Lys Leu V 5	al Thr Cys A 10	asp Phe Cys Lys Arg Asp Asp 15
Ile Lys L	ys Lys Glu Le 20	eu Glu Thr Hi 25 28	s Tyr Lys Thr Cys
(2) INFOI	RMATION FO	OR SEQ ID N	IO:16:
(A) L (B) T	UENCE CHA ENGTH: 26 a YPE: Amino OPOLOGY: I	mino acids Acid	TICS:
(xi) SEQ	UENCE DES	CRIPTION:	SEQ ID NO:16:
Gln Asp 1	Leu Ala Val C 5	Cys Asp Val (10	Cys Asn Arg Lys Phe Arg His 15
Lys Asp	Гуг Leu Arg A 20	Asp His Gln I 25 26	ys Thr His
(2) INFOI	RMATION FO	OR SEQ ID N	IO:17:



	-	HARACTE			
` '		28 amino ac	ids		
` ,	TYPE: Ami				
(D)	TOPOLOG	Y: Linear			
(xi) SE	QUENCE I)ESCRIPTIO	ON: SEQ	ID NO:17:	
Thr Gly	Lys Tyr Pro	o Phe Ile Cy 10	s Ser Glu 15	Cys Gly Lys Se	r Phe
Met Asp	Lys Arg T 20	yr Leu Lys 1 25	lle His Sei 28	Asn Val His	
(2) INFO	RMATION	FOR SEQ	ID NO:18	:	
(i) SEC	DUENCE C	HARACTE	RISTICS:		
	-	28 amino aci			
` '	TYPE: Ami				
` '	TOPOLOG				
(xi) SE	QUENCE D	ESCRIPTION	ON: SEQ	ID NO:18:	
Thr Gly	Glu Lys Pro	o Tyr Thr C	ys Thr Va 15	l Cys Gly Lys L	ys Phe
Ile Asp	Arg Ser Ser 20	Val Val Ly 25	s His Ser A	Arg Thr His	
(2) INFO	RMATION	FOR SEQ	ID NO:19	:	
(i) SEC	DUENCE C	HARACTE	RISTICS:		
• • •	-	28 amino aci			
	ΓΥΡΕ: Ami		.45		
, ,	TOPOLOG				
(xi) SE	QUENCE D	ESCRIPTION OF THE PROPERTY OF	ON: SEQ	ID NO:19:	
Arg Lys	Lys Phe Pr 5	o His Ile Cy 10	s Gly Glu 15	Cys Gly Lys Gl	y Phe



Pro Ser Ala Lo 20	eu Lys Ly 25	ys His II 28	e Arg Val H	His
RMATION F	OR SEQ	ID NO:	20:	
ENGTH: 28 a	amino aci Acid		S:	
UENCE DES	SCRIPTIO	ON: SE	Q ID NO:20) :
Glu Lys Pro P 5	he Glu C	•		Lys Lys Phe
Ala Arg His L 20	Leu Val L 25	ys His (28	Gln Arg Ile	His
RMATION F	OR SEQ	ID NO:	21:	
ENGTH: 28 a YPE: Amino	amino aci Acid		S:	
UENCE DES	SCRIPTIO	ON: SEC	Q ID NO:21	:
Glu Gln Met A 5	Ala Gln C 10	•	•	Gln Phe Tyr
•	•		eu Asp Glu	ı Cys
RMATION FO	OR SEQ	ID NO:2	22:	
ENGTH: 28 a YPE: Amino	amino aci Acid		S:	
UENCE DES	CRIPTIC	ON: SEC	Q ID NO:22	:
	RMATION F UENCE CHAENGTH: 28 a YPE: Amino OPOLOGY: UENCE DES Glu Lys Pro P 5 Ala Arg His I 20 RMATION F UENCE CHAENGTH: 28 a YPE: Amino OPOLOGY: UENCE DES Glu Gln Met A 5 Lys Ala Leu C 20 RMATION F UENCE CHAENGTH: 28 a YPE: Amino OPOLOGY:	RMATION FOR SEQ UENCE CHARACTE ENGTH: 28 amino aci YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION Glu Lys Pro Phe Glu C 5 10 Ala Arg His Leu Val L 20 25 RMATION FOR SEQ UENCE CHARACTE ENGTH: 28 amino aci YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION Glu Gln Met Ala Gln C 5 10 Lys Ala Leu Glu Lys T 20 25 RMATION FOR SEQ UENCE DESCRIPTION UENCE DESCRIPTION UENCE DESCRIPTION UENCE DESCRIPTION UENCE DESCRIPTION UENCE DESCRIPTION UENCE CHARACTE UENCE	RMATION FOR SEQ ID NO: UENCE CHARACTERISTICS ENGTH: 28 amino acids YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION: SEC Glu Lys Pro Phe Glu Cys Glu C 5 10 15 Ala Arg His Leu Val Lys His C 20 25 28 RMATION FOR SEQ ID NO: UENCE CHARACTERISTICS ENGTH: 28 amino acids YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION: SEC Glu Gln Met Ala Gln Cys Pro I 5 10 15 Lys Ala Leu Glu Lys Thr His L 20 25 28 RMATION FOR SEQ ID NO: UENCE DESCRIPTION: SEC UENCE DESCRIPTION: SEC Glu Gln Met Ala Gln Cys Pro I 5 10 15 Lys Ala Leu Glu Lys Thr His L 20 25 28 RMATION FOR SEQ ID NO: UENCE CHARACTERISTICS ENGTH: 28 amino acids YPE: Amino Acid OPOLOGY: Linear	RMATION FOR SEQ ID NO:20: UENCE CHARACTERISTICS: ENGTH: 28 amino acids YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION: SEQ ID NO:20 Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly 5 10 15 Ala Arg His Leu Val Lys His Gln Arg Ile 1 20 25 28 RMATION FOR SEQ ID NO:21: UENCE CHARACTERISTICS: ENGTH: 28 amino acids YPE: Amino Acid OPOLOGY: Linear UENCE DESCRIPTION: SEQ ID NO:21 Glu Gln Met Ala Gln Cys Pro Ile Cys Gln 5 10 15 Lys Ala Leu Glu Lys Thr His Leu Asp Glu 20 25 28 RMATION FOR SEQ ID NO:22: UENCE CHARACTERISTICS: ENGTH: 28 amino acids YPE: Amino Acid

Pro A	sp Asp Gly I	Leu Val Ala Cy	s Pro Ile Cy	s Leu Thr Arg Met
1	5	10	15	

Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys 20 25 28

- (2) INFORMATION FOR SEQ ID NO:23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTTGTGCCT GCAGAGAGAA G 21

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGGTTAAC TTTCGGTGCT CCCCAGCAGG GTCTC 35

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

(28

CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35

- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGGTTAAC TGCACTGGCC GAGCTCTCCA GGGA 34

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
- **GTGATGAGAA TTCAT 15**
- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
- **CGATGAATTC TCATCACTGC A 21**
- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
- GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33
- (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCTGGTTAA CTGGGC 16

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCNCCNATGG CNYTNGARC 19

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCNCCNATGG CNYTNGARA 19

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCCNATGG CNYTNGARG 19

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CYTCNARNGC CATNGGNGC 19

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AARCAYGCNT AYGTNAA 17

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTNACRTANG CRTGYTT 17

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala Pro Met Ala Leu Glu Arg 1 5 7
(2) INFORMATION FOR SEQ ID NO:42:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 6 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
Lys His Ala Tyr Val Lys 1 5 6
(2) INFORMATION FOR SEQ ID NO:43:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 7 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
Pro Gly Ser Asn Leu Gly Ser 1 5 7
(2) INFORMATION FOR SEQ ID NO:44:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 8 amino acids(B) TYPE: Amino Acid(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
Lys Asp Asp Thr Met Phe Leu Lys 1 5 8
(2) INFORMATION FOR SEQ ID NO:45:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs(B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs



(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single



- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGGATCC GGAGACACAG ATTCCAGCCC C 31

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGAATTC TTAACTCTTC GGTGCTCCCC AGCAG 35

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGGCTGGC CTAATGT 17

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCTGGCGAA GAAGTCC 17

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 31

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30

SEQUENCE LISTING

(1) GENERAL	INFORMATION:
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- 5 (i) APPLICANT: Goeddel, David V. Rothe, Mike
 - (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
- 10 (iii) NUMBER OF SEQUENCES: 62
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 460 Point San Bruno Blvd
- 15 (C) CITY: South San Francisco
 - (D) STATE: California (E) COUNTRY: USA
 - (F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: patin (Genentech)
- 25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 27-May-1994
 - (C) CLASSIFICATION:
- 30
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dreger, Ginger R.
 - (B) REGISTRATION NUMBER: 33,055
 - (C) REFERENCE/DOCKET NUMBER: 897
- 40 (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/225-3216
 - (B) TELEFAX: 415/952-9881
 - (C) TELEX: 910/371-7168
- 45 (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 bases

(B) TYPE: nucleic acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCCATC 300 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700

CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800 ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900 GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350 CGGCTGCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400 CCTACGTCAA AGATGACACA ATGTTCCTCA AATGCATTGT GGACACTAGT 1450 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500

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	GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1990
5	CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600
	GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650
10	GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700
	GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750
15	GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800
20	AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850
	TGGAAAAATG CCCCCATCTC TCTGTTCAGA CTCAAAACTA GAACCACAGG 1900
25	GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950
	CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000
30	TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050
35	ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAA 2088

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly 1 5 10 15

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	Cys Pro Pro	Ala Pro Cys Gl 20	n Asp Pro Ser G 25	ilu Pro Arg Val Leu 30
5	Cys Cys Th	r Ala Cys Leu S 35	èr Glu Asn Leu 40	Arg Asp Asp Glu As 45
	Arg Ile Cys	Pro Lys Cys Arg 50	g Ala Asp Asn L 55	eu His Pro Val Ser 60
10	Pro Gly Ser	Pro Leu Thr Glr 65	n Glu Lys Val Hi 70	s Ser Asp Val Ala 75
1 5	Glu Ala Glu	lle Met Cys Pro 80	Phe Ala Gly Va 85	al Gly Cys Ser Phe 90
15	Lys Gly Ser	Pro Gln Ser Me 95	t Gln Glu His G 100	lu Ala Thr Ser Gln 105
20		Leu Tyr Leu Le 110	u Leu Ala Val Le 115	eu Lys Glu Trp Lys 120
		Gly Ser Asn Le 125	u Gly Ser Ala P 130	ro Met Ala Leu Glu 135
25		ı Ser Glu Leu G 140	in Leu Gin Ala / 145	Ala Val Glu Ala Thr 150
30		ı Glu Val Asp C 155	ys Tyr Arg Ala 160	Pro Cys Cys Glu Ser 165
30		Leu Ala Leu Gi 170	n His Leu Val L 175	ys Glu Lys Leu Leu 180
35	Ala Gln Leu	Glu Glu Lys Le 185	u Arg Val Phe A 190	Ala Asn Ile Val Ala 195
		n Lys Glu Val G 200	lu Ala Ser His Lo 205	eu Ala Leu Ala Ala 210
40		Gin Ser Gin Leu 215	Asp Arg Glu Hi 220	s Leu Leu Ser Leu 225
45	Glu Gln Arg	y Val Val Glu Le 230	u Gln Gln Thr L 235	eu Ala Gin Lys Asp 240
70	Gin Val Leu	Gly Lys Leu G 245	lu His Ser Leu A 250	arg Leu Met Glu Glu 255

	Ala Ser Phe Asp Gly Thr Phe Let 260 265				
5	Lys Arg Cys His Glu Ser Val Cys 275 280	· -			
	Ser Pro Ala Phe Tyr Thr Ala Lys 290 295				
10	Arg Leu Tyr Leu Asn Gly Asp Gl 305 310				
15	Ser Leu Phe Ile Val Ile Met Arg (320 325				
	Pro Trp Pro Phe Arg Asn Lys Va 335 340	· ·			
20	Asn Asn Arg Glu His Ala Ile Asp 350 355	· · · · · · · · · · · · · · · · · · ·			
	Ser Ala Ser Phe Gln Arg Pro Gln 365 370				
25	Gly Cys Pro Leu Phe Phe Pro Leu 380 385	•			
30	His Ala Tyr Val Lys Asp Asp Th 395 400				
	Asp Thr Ser Ala 409				
35	(2) INFORMATION FOR SEQ ID NO:3:				
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2121 bases (B) TYPE: nucleic acid				
40	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	;			
	(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:3:			
45	GCGCGAAGAC CGTTGGGGCT	TTGTGGTGTG TGGGGGTTGT AACTCAC	ATG 50		
	GCTGCAGCCA GTGTGACTTC	CCCTGGCTCC CTAGAACTGC TACAGCC	TGG 100		

CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150 CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200 CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250 CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300 TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCGCAG AGAGGTGGAG 350 AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400 GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450 AGTGTCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550 ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650 TTTCAGGACC ATGTTAGAGC ATGCAGCAAA TGCCGGGTTC TCTGCAGATT 700 CCACACCGTT GGCTGTTCAG AGATGGTGGA GACTGAGAAC CTGCAGGATC 750 ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800 TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900

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TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000 TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050 TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100 **GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150** CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200 GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250 GGGCGGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300 TGATGCTCTG TTGCAGTGGC CTTTTAATCA GAAGGTAACA TTGATGTTGC 1350 TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400 ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450 CTGCCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500 TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550 TAGCCACCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600 CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650 GGAGGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700

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	AGCCTCCAGT TGGCCTTCAG CTGGCAAACT GAGTTGGACG GTCCACTGAG 1750
5	CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800
	AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGC CTGTAGGTGG 1850
10	GTGCTCAGAA AGGGCCTCTC CAGAGAGAT CTCAAGAGCT GCAGCAGGAG 1900
	CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950
15	ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000
20	CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050
	TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100
25	CGACAAAAA AAAAAAAAA A 2121

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu

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Gin Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala

Lys Tyr Leu Cys Ser Ala Cys Lys Asn lle Leu Arg Arg Pro Phe 40 45 35

Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser

	lle Leu Ser	Ser Gly Pro Gln 65	Asn Cys Ala Ala 70	ı Cys Val Tyr Glu 75
5	Gly Leu Tyr	Glu Glu Gly Ile 80	Ser Ile Leu Glu 9 85	Ser Ser Ala 90
	Phe Pro As	p Asn Ala Ala A 95	rg Arg Glu Val G 100	ilu Ser Leu Pro Ala 105
10	Val Cys Pro	Asn Asp Gly C 110	ys Thr Trp Lys (115	Gly Thr Leu Lys Glu 120
15	Tyr Glu Ser	Cys His Glu Gl 125	y Leu Cys Pro Pł 130	ne Leu Leu Thr Glu 135
13	Cys Pro Ala	a Cys Lys Gly Le 140	eu Val Arg Leu S 145	er Glu Lys Glu His 150
20	His Thr Glu	Gln Glu Cys Pro 155	o Lys Arg Ser Le 160	u Ser Cys Gln His 165
,	Cys Arg Ala	a Pro Cys Ser H 170	is Val Asp Leu G 175	ilu Val His Tyr Glu 180
25	Val Cys Pro	Lys Phe Pro Le 185	u Thr Cys Asp (190	Gly Cys Gly Lys Lys 195
30	Lys lle Pro	Arg Glu Thr Phe 200	GIn Asp His Va 205	l Arg Ala Cys Ser 210
30	Lys Cys Ar	g Val Leu Cys A 215	arg Phe His Thr \ 220	/al Gly Cys Ser Glu 225
35	Met Val Gl	ı Thr Glu Asn L 230	eu Gln Asp His (235	Glu Leu Gln Arg Leu 240
	Arg Glu His	s Leu Ala Leu Le 245	eu Leu Ser Ser Pl 250	he Leu Glu Ala Gln 255
40	Ala Ser Pro	Gly Thr Leu As 260	an Gin Val Gly Pr 265	o Glu Leu Leu Gln 270
45	Arg Cys Gl	n lle Leu Glu Gli 275	n Lys lle Ala Thr 280	Phe Glu Asn Ile 285
.5	Val Cys Va	l Leu Asn Arg G 290	Glu Val Glu Arg V 295	/al Ala Val Thr Ala 300

	Glu Ala Cy	s Ser Arg Gln Hi 305	s Arg Leu Asp 0 310	iln Asp Lys Ile Glu 315
5	Ala Leu Se	r Asn Lys Val Gl 320	n Gln Leu Glu A 325	rg Ser lle Gly Leu 330
	Lys Asp Le	eu Ala Met Ala A 335	sp Leu Glu Gln 340	Lys Val Ser Glu Leu 345
10	Glu Val Se	r Thr Tyr Asp Gl 350	y Val Phe lle Trp 355	Lys Ile Ser Asp 360
15	Phe Thr Ar	g Lys Arg Gln G 365	lu Ala Val Ala G 370	y Arg Thr Pro Ala 375
13	lle Phe Ser	Pro Ala Phe Tyr 380	Thr Ser Arg Tyl 385	Gly Tyr Lys Met 390
20	Cys Leu Ai	rg Val Tyr Leu A 395	sn Gly Asp Gly [*] 400	Thr Gly Arg Gly Thi 405
	His Leu Se	r Leu Phe Phe V 410	al Val Met Lys G 415	ily Pro Asn Asp Ala 420
25	Leu Leu Gl	n Trp Pro Phe As 425	sn Gin Lys Val T 430	hr Leu Met Leu Leu 435
30	Asp His As	sn Asn Arg Glu H 440	lis Val IIe Asp A 445	la Phe Arg Pro Asp 450
30	Val Thr Se	r Ser Ser Phe Gli 455	n Arg Pro Val Se 460	er Asp Met Asn IIe 465
35	Ala Ser Gly	/ Cys Pro Leu Ph 470	ie Cys Pro Val S 475	er Lys Met Glu Ala 480
	Lys Asn Se	er Tyr Val Arg A 485	sp Asp Ala lle Pi 490	ne lle Lys Ala lle 495
40	Val Asp Le	u Thr Gly Leu 500 501		
	(2) INFORM	NATION FOR SEC	2 ID NO:5:	
45	(A) LE (B) TY	ENCE CHARACT NGTH: 44 amino PE: amino acid		

5	Asp Leu Lei	Cys Pro Ile Cy 5	s Met Gin Ile 10	lle Lys Asp Ala Phe 15
5	Leu Thr Ala	Cys Gly His Se 20	r Phe Cys Tyr 25	Met Cys IIe IIe Thr 30
10	His Leu Arg	Asn Lys Ser A		s Cys Ser Gln His 44
	(2) INFORM	ATION FOR SEC	1D NO:6:	
15	(A) LEN (B) TYP	NCE CHARACTI GTH: 47 amino E: amino acid POLOGY: linear		
20	(xi) SEQUE	NCE DESCRIPT	ION: SEQ ID N	NO:6:
20	Glu Leu Ser 1	Cys Ser Ile Cys 5	Leu Glu Pro l 10	Phe Lys Glu Pro Val 15
25	Thr Thr Pro	Cys Gly His As 20	n Phe Cys Gly 25	Ser Cys Leu Asn Glu 30
	Thr Trp Ala	Val Gln Gly Ser 35	Pro Tyr Leu (Cys Pro Gln Cys Arg 45
30	Ala Val 47			
	(2) INFORMA	ATION FOR SEC	1D NO:7:	
35	(A) LEN (B) TYP	NCE CHARACTI GTH: 44 amino E: amino acid POLOGY: linear		
10	(xi) SEQUE	NCE DESCRIPT	ION: SEQ ID N	10:7:
	Leu Leu Arg	Cys His IIe Cys 5	s Lys Asp Phe 10	Leu Lys Val Pro Val 15
15	Leu Thr Pro	Cys Gly His Th 20	r Phe Cys Ser 25	Leu Cys Ile Arg Thr 30
	His Leu Asn	Asn Gln Pro A	sn Cys Pro Le	u Cys Leu Phe Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: 5 (A) LENGTH: 44 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: 10 Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met 5 10 1 Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg 15 25 Cys Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr 40 44 20 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: amino acid 25 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val 30 5 10 1 Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg 25 20 35 Cys Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro 35 40 45 40 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 amino acids (B) TYPE: amino acid 45 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40

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	Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val 1 5 10 15
5	Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln 20 25 30
	Val Gly Lys Gly Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg 35 40 45
10	(2) INFORMATION FOR SEQ ID NO:11:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
20	Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met 1 5 10 15
25	Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys lle Val 20 25 30
23	Thr Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys 35 40 45
30	Lys 46
	(2) INFORMATION FOR SEQ ID NO:12:
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
	Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val 1 5 10 15
45	Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu 20 25 30
	Asn Tyr Glu Ser Asn Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro 35 40 45

50 (2) INFORMATION FOR SEQ ID NO:13: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 47 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Glu Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met 10 15 15 Met Leu Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg 25 Cys Trp Gly Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg 40 20 35 Glu Thr 47 (2) INFORMATION FOR SEQ ID NO:14: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: Phe Gin Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys 10 35 lle Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser 25 Trp Gln Glu Ser Glu Gly Gln Gly Ser Ser Gly Cys Pro Phe Cys 40 45 40 35 Arg Cys Glu 48 45 (2) INFORMATION FOR SEQ ID NO:15:

Val Cys Arg Val Pro

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: 5 Gly Gly Phe Lys Leu Val Thr Cys Asp Phe Cys Lys Arg Asp Asp 5 10 15 1 lle Lys Lys Glu Leu Glu Thr His Tyr Lys Thr Cys 10 20 25 28 (2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: 15 (A) LENGTH: 26 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: 20 Gln Asp Leu Ala Val Cys Asp Val Cys Asn Arg Lys Phe Arg His 10 Lys Asp Tyr Leu Arg Asp His Gln Lys Thr His 25 20 25 26 (2) INFORMATION FOR SEQ ID NO:17: (i) SEQUENCE CHARACTERISTICS: 30 (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: 35 Thr Gly Lys Tyr Pro Phe IIe Cys Ser Glu Cys Gly Lys Ser Phe 10 15 1 5 40 Met Asp Lys Arg Tyr Leu Lys Ile His Ser Asn Val His 28 20 25 (2) INFORMATION FOR SEQ ID NO:18: 45 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
5	Thr Gly Glu Lys Pro Tyr Thr Cys Thr Val Cys Gly Lys Lys Phe 1 5 10 15
	lle Asp Arg Ser Ser Val Val Lys His Ser Arg Thr His 20 25 28
10	(2) INFORMATION FOR SEQ ID NO:19:
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
20	Arg Lys Lys Phe Pro His IIe Cys Gly Glu Cys Gly Lys Gly Phe 1 5 10 15
20	Arg His Pro Ser Ala Leu Lys Lys His Ile Arg Val His 20 25 28
25	(2) INFORMATION FOR SEQ ID NO:20:
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
35	Ser Glu Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly Lys Lys Phe 1 5 10 15
	Arg Thr Ala Arg His Leu Val Lys His Gln Arg Ile His 20 25 28
40	(2) INFORMATION FOR SEQ ID NO:21:
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
•	Pro Asn Glu Gln Met Ala Gln Cys Pro Ile Cys Gln Gln Phe Tyr

10 15 5 1 Pro Leu Lys Ala Leu Glu Lys Thr His Leu Asp Glu Cys 25 28 5 (2) INFORMATION FOR SEQ ID NO:22: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 amino acids (B) TYPE: amino acid 10 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22: Pro Asp Asp Gly Leu Val Ala Cys Pro Ile Cys Leu Thr Arg Met 15 10 Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys 25 20 (2) INFORMATION FOR SEQ ID NO:23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases 25 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: 30 **CCTTGTGCCT GCAGAGAGAA G 21** 35 (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid 40 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 45 CTAGGTTAAC TTTCGGTGCT CCCCAGCAGG GTCTC 35

	(2) INFORMATION FOR SEQ ID NO:25:
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
	CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35
15	
	(2) INFORMATION FOR SEQ ID NO:26:
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
	CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35
30	•
	(2) INFORMATION FOR SEQ ID NO:27:
35	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
45	CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35
	(2) INFORMATION FOR SEQ ID NO:28:

5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
10	CTAGGTTAAC TGCACTGGCC GAGCTCTCCA GGGA 34
15	(2) INFORMATION FOR SEQ ID NO:29:
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 15 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
25	GTGATGAGAA TTCAT 15
30	(2) INFORMATION FOR SEQ ID NO:30:
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single
35	(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
40	CGATGAATTC TCATCACTGC A 21
45	(2) INFORMATION FOR SEQ ID NO:31:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 bases (B) TYPE: nucleic acid

	(D) TOPOLOGY: linear
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
	GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33
10	(2) INFORMATION FOR SEQ ID NO:32:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
	GCCTGGTTAA CTGGGC 16
25	(2) INFORMATION FOR SEQ ID NO:33:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
	GCNCCNATGG CNYTNGARC 19
40	(2) INFORMATION FOR SEQ ID NO:34:
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(C) STRANDEDNESS: single

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
5	GCNCCNATGG CNYTNGARA 19
	(2) INFORMATION FOR SEQ ID NO:35:
10	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
20	GCNCCNATGG CNYTNGARG 19
	(2) INFORMATION FOR SEQ ID NO:36:
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single
30	(D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
35	GYTCNARNGC CATNGGNGC 19
	(2) INFORMATION FOR SEQ ID NO:37:
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single
45	(D) TOPOLOGY: linear

TYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:38:

10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
15	CYTCNARNGC CATNGGNGC 19
20	(2) INFORMATION FOR SEQ ID NO:39:
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
30	AARCAYGCNT AYGTNAA 17
3.5	(2) INFORMATION FOR SEQ ID NO:40:
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
45	TTNACRTANG CRTGYTT 17

	(2) INFORMATION FOR SEQ ID NO:41:
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
10	Pro Gly Ser Asn Leu Gly Ser 1 5 7
	(2) INFORMATION FOR SEQ ID NO:42:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
	Lys Asp Asp Thr Met Phe Leu Lys 1 5 8
25	(2) INFORMATION FOR SEQ ID NO:43:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
35	Pro Gly Ser Asn Leu Gly Ser 1 5 7
	(2) INFORMATION FOR SEQ ID NO:44:
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
45	Lys Asp Asp Thr Met Phe Leu Lys

	(2) INFORMATION FOR SEQ ID NO:45:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	,
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
	TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37	
15	(2) INFORMATION FOR SEQ ID NO:46:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	•
	CTAGAGATCT CAGGGGTCAG GCCACTTT 28	
30	(2) INFORMATION FOR SEQ ID NO:47:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
	CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41	
45	(2) INFORMATION FOR SEQ ID NO:48:	,
	(i) SEQUENCE CHARACTERISTICS:	

_	(A) LENGTH: 41 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
10	CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41
	(2) INFORMATION FOR SEQ ID NO:49:
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
25	CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41
	(2) INFORMATION FOR SEQ ID NO:50:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
40	TCGATCGTCG ACCAAAAGA AGCCCTCCTG CCTACAA 37
	(2) INFORMATION FOR SEQ ID NO:51:
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 28 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
5	CTAGAGATCT CAGGGGTCAG GCCACTTT 28
LO	(2) INFORMATION FOR SEQ ID NO:52:
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
20	TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34
25	(2) INFORMATION FOR SEQ ID NO:53:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
35	GATCGGATCC GGAGACACAG ATTCCAGCCC C 31
40	(2) INFORMATION FOR SEQ ID NO:54:
4 5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGAATTC TTAACTCTTC GGTGCTCCCC AGCAG 35

5	(2) INFORMATION FOR SEQ ID NO:55:
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
	GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30
20	(2) INFORMATION FOR SEQ ID NO:56:
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
	CCTGGCTGGC CTAATGT 17
35	(2) INFORMATION FOR SEQ ID NO:57:
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
	GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

5	(2) INFORMATION FOR SEQ ID NO:58:
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
15	CTCTGGCGAA GAAGTCC 17
20	(2) INFORMATION FOR SEQ ID NO:59:
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
30	GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 3
35	(2) INFORMATION FOR SEQ ID NO:60:
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
45	GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

	(2) INFORMATION FOR SEQ ID NO:61:
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
	GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30
15	(2) INFORMATION FOR SEQ ID NO:62:
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
	GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30